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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/038,937

DATE: 05/14/2002

TIME: 15:00:19

Input Set : N:\Crf3\RULE60\10038937.txt

Output Set: N:\CRF3\05142002\J038937.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Daggett, Lorrie P.

6 Lu, Chin-Chun

9 (ii) TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR

10 SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR

12 (iii) NUMBER OF SEQUENCES: 63

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Heller Ehrman White & McAuliffe

16 (B) STREET: 4250 Executive Square, 7th Floor

17 (C) CITY: La Jolla

18 (D) STATE: CA

19 (E) COUNTRY: U.S.A.

20 (F) ZIP: 92037

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk

24 (B) COMPUTER: IBM PC compatible

25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/10/038,937

C--> 30 (B) FILING DATE: 18-Apr-2002

45 (C) CLASSIFICATION:

42 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: 08/935,105

34 (B) FILING DATE: 29-SEPT-97

38 (A) APPLICATION NUMBER: US 08/231,193

39 (B) FILING DATE: 20-APR-1994

43 (A) APPLICATION NUMBER: US 08/052,449

44 (B) FILING DATE: 20-APR-1993

47 (viii) ATTORNEY/AGENT INFORMATION:

48 (A) NAME: Seidman, Stephanie

49 (B) REGISTRATION NUMBER: 33,779

50 (C) REFERENCE/DOCKET NUMBER: 6362-9383D

52 (ix) TELECOMMUNICATION INFORMATION:

53 (A) TELEPHONE: 619-238-0999

54 (B) TELEFAX: 619-238-0062

57 (2) INFORMATION FOR SEQ ID NO: 1:

59 (i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 4298 base pairs

61 (B) TYPE: nucleic acid

62 (C) STRANDEDNESS: both

63 (D) TOPOLOGY: both

ENTERED

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65      (ii) MOLECULE TYPE: cDNA
68      (ix) FEATURE:
69          (A) NAME/KEY: CDS
70          (B) LOCATION: 262..3078
72      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
74 CAAGCCGGGGC GTTCGGAGCT GTGCCCAGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG 60
76 CGTGGGGCTG AGCGCCGAGC CCCCAGCAC GCTTCAGCCC CCGTCCCTC GGCCGACGIC 120
78 CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGAGCC CCGGGGGCCG GCGAGAGCGA 180
80 GGACGGCCCG GAAGCCCCGC GGGGGATGGC CCGAGGGCCC CCGCTTCGCG CCGCGCAGAG 240
82 CCAGGCCCCG GGGCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC 291
83                               Met Ser Thr Met Arg Leu Leu Thr Leu Ala
84                               1           5           10
86 CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC 339
87 Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile
88                               15           20           25
90 GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC 387
91 Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe
92                               30           35           40
94 CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT 435
95 Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile
96                               45           50           55
98 CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG 483
99 Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met
100                               60           65           70
102 GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC 531
103 Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile
104 75                               80           85           90
106 CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT 579
107 Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro
108                               95           100          105
110 GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC 627
111 Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr
112                               110          115          120
114 ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG 675
115 Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu
116                               125          130          135
118 CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG 723
119 Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met
120                               140          145          150
122 ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC 771
123 Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp
124 155                               160          165          170
126 CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG 819
127 His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu
128                               175          180          185
130 CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG 867
131 Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys
132                               190          195          200
134 AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC 915

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```

135 Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val
136      205      210      215
138 ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC ACT GTA TAC CGC GCA      963
139 Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala
140      220      225      230
142 GCC GCG ATG CTG AAC ATG ACG GGC TCC GGG TAC GTG TGG CTG GTC GGC      1011
143 Ala Ala Met Leu Asn Met Thr Gly Ser Gly Tyr Val Trp Leu Val Gly
144 235      240      245      250
147 GAG CGC GAG ATC TCG GGG AAC GCC CTG CGC TAC GCC CCA GAC GGC ATC      1059
148 Glu Arg Glu Ile Ser Gly Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile
149      255      260      265
151 CTC GGG CTG CAG CTC ATC AAC GGC AAG AAC GAG TCG GCC CAC ATC AGC      1107
152 Leu Gly Leu Gln Leu Ile Asn Gly Lys Asn Glu Ser Ala His Ile Ser
153      270      275      280
155 GAC GCC GTG GGC GTG GTG GCC CAG GCC GTG CAC GAG CTC CTC GAG AAG      1155
156 Asp Ala Val Gly Val Val Ala Gln Ala Val His Glu Leu Leu Glu Lys
157      285      290      295
159 GAG AAC ATC ACC GAC CCG CCG GGC TGC GTG GGC AAC ACC AAC ATC      1203
160 Glu Asn Ile Thr Asp Pro Pro Arg Gly Cys Val Gly Asn Thr Asn Ile
161      300      305      310
163 TGG AAG ACC GGG CCG CTC TTC AAG AGA GTG CTG ATG TCT TCC AAG TAT      1251
164 Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr
165 315      320      325      330
167 GCG GAT GGG GTG ACT GGT CCG GTG GAG TTC AAT GAG GAT GGG GAC CGG      1299
168 Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg
169      335      340      345
171 AAG TTC GCC AAC TAC AGC ATC ATG AAC CTG CAG AAC CGC AAG CTG GTG      1347
172 Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val
173      350      355      360
175 CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC CCT AAT GAC AGG AAG      1395
176 Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys
177      365      370      375
179 ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT CGA GGG TAC CAG ATG      1443
180 Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met
181      380      385      390
183 TCC ACC AGA CTG AAG ATT GTG ACG ATC CAC CAG GAG CCC TTC GTG TAC      1491
184 Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr
185 395      400      405      410
187 GTC AAG CCC ACG CTG AGT GAT GGG ACA TGC AAG GAG GAG TTC ACA GTC      1539
188 Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val
189      415      420      425
191 AAC GGC GAC CCA GTC AAG AAG GTG ATC TGC ACC GGG CCC AAC GAC ACG      1587
192 Asn Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr
193      430      435      440
195 TCG CCG GGC AGC CCC CGC CAC ACG GTG CCT CAG TGT TGC TAC GGC TTT      1635
196 Ser Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Tyr Gly Phe
197      445      450      455
199 TGC ATC GAC CTG CTC ATC AAG CTG GCA CGG ACC ATG AAC TTC ACC TAC      1683
200 Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr

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file:///C:/Crf3/Outhold/VsrJ038937.htm

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```

267 TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC CTG 2499
268 Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu
269 735 740 745
271 GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC ATG 2547
272 Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met
273 750 755 760
275 CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC AAG 2595
276 Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys
277 765 770 775
279 TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CGG 2643
280 Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg
281 780 785 790
283 TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CIT ACT TTT 2691
284 Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe
285 795 800 805 810
287 GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG GCC 2739
288 Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala
289 815 820 825
291 GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG GAT 2787
292 Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp
293 830 835 840
295 GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG TGG 2835
296 Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp
297 845 850 855
299 CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC CCT 2883
300 Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro
301 860 865 870
303 AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC 2931
304 Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser
305 875 880 885 890
307 TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG AGC ACC GGG GGT GGA CGC 2979
308 Phe Lys Arg Arg Ser Ser Lys Asp Thr Ser Thr Gly Gly Gly Arg
309 895 900 905
311 GGT GCT TTG CAA AAC CAA AAA GAC ACA GTG CTG CCG CGA CGC GCT ATT 3027
312 Gly Ala Leu Gln Asn Gln Lys Asp Thr Val Leu Pro Arg Arg Ala Ile
313 910 915 920
315 GAG AGG GAG GAG GGC CAG CTG CAG CTG TGT TCC CGT CAT AGG GAG AGC 3075
316 Glu Arg Glu Glu Gly Gln Leu Gln Leu Cys Ser Arg His Arg Glu Ser
317 925 930 935
319 TGAGACTCCC CGCCCCCCTT CCTCTGCCCC CCCCCCGCA GACAGACAGA CAGACGGACG 3135
321 GGACAGCGGC CCGGCCACG CAGAGCCCCG GAGCAACACG GGGTCGGGGG AGGAGCACCC 3195
323 CCAGCCTCCC CCAGGCTGCG CCTGCCCGCC CGCCGGTTGG CCGGCTGGCC GGTCCACCCC 3255
325 GTCCCGGCCC CGCGCGTGCC CCCAGCGTGG GGCTAACGGG CGCCTTGTCT GTGTATTTCT 3315
327 ATTTTGCAGC AGTACCATCC CACTGATAIC ACGGGCCCCG TCAACCTCTC AGATCCCTCG 3375
329 GTCAGCACCG TGGTGTGAGG CCCCCGAGG CGCCACCTG CCCAGTTAGC CCGGCCAAGG 3435
331 ACACTGATGG GTCTCTGTC TCGGGAAGGC CTGAGGGAAG CCCACCCGCC CCAGAGACTG 3495
333 CCCACCCTGG GCCTCCCGTC CGTCCGCCCG CCCACCCCGC TGCTTGGCGG GCAGCCCTG 3555
335 CTGGACCAAG GTGCGGACCG GAGCGGCTGA GGACGGGGCA GAGCTGAGTC GGCTGGGCAG 3615
337 GGCCGCAGGG CGCTCCGGCA GAGGCAGGCC CCTGGGGTCT CTGAGCAGTG GGGAGCGGGG 3675

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/038,937

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Input Set : N:\Crf3\RULE60\10038937.txt  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:45; N Pos. 18  
Seq#:47; N Pos. 18  
Seq#:49; N Pos. 18  
Seq#:51; N Pos. 18  
Seq#:53; N Pos. 18  
Seq#:57; Xaa Pos.1147,1171  
Seq#:58; Xaa Pos.1147,1171

## VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10038937.txt

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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:1631 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10  
L:2123 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13  
L:2127 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13  
L:2131 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13  
L:2135 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13  
L:2139 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13  
L:2143 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13  
L:2147 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13  
L:2151 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13  
L:2155 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13  
L:2159 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13  
L:2163 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13  
L:2167 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13  
L:2171 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13  
L:2175 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13  
L:2179 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13  
L:2183 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13  
L:2187 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13  
L:2191 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13  
L:2195 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13  
L:2199 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13  
L:4013 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:4017 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:4021 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:4025 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:4029 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:4033 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:4037 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:4041 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:4045 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:4049 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:4053 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:4057 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:4061 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:4065 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:4069 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:4073 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:4077 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:4081 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:4085 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:4089 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:4093 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:4097 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:4101 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:4105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:4109 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23

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Input Set : N:\Crf3\RULE60\10038937.txt

Output Set: N:\CRF3\05142002\J038937.raw

L:4375 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25  
L:4379 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25  
L:4383 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25  
L:4387 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25  
L:12994 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:3937  
L:13002 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:4033  
L:13277 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:1136  
L:13283 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:1168